

Slobodyan

1652 RUSH

#5

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/952,741

DATE: 09/11/98
TIME: 15:49:27

Input Set: H952741.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

new format

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1 <110> APPLICANT: Yuji, HATADA
2 Katsuya, OZAKI
3 Katsutoshi, ARA
4 Shuji, KAWAI
5 Susumu, ITO
6 <120> TITLE OF INVENTION: GENE ENCODING ALKALINE LIQUEFYING ALPHA-AMYLASE
7 <130> FILE REFERENCE: 2173-106P
8 <140> CURRENT APPLICATION NUMBER: US/08/952,741
9 <141> CURRENT FILING DATE: 1997-11-25
10 <160> NUMBER OF SEQ ID NOS: 11
11 <170> SOFTWARE: PatentIn Ver. 2.0
12 <210> SEQ ID NO 1
13 <211> LENGTH: 1776
14 <212> TYPE: DNA
15 <213> ORGANISM: Bacillus sp.
16 <220> FEATURE:
17 <221> NAME/KEY: CDS
18 <222> LOCATION: (145)..(1692)
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21 ttgggagtta ggaagtata ttaaaggatt ttttttgact tgttgtgaaa acgcttgcat 120
22 aaattgaagg agaggggtgct tttt atg aaa ctt cat aac cgt ata att agc 171
23 Met Lys Leu His Asn Arg Ile Ile Ser
24 1 5
25 gta cta tta aca cta ttg tta gct gta gct gtt ttg ttt cca tat atg 219
26 Val Leu Leu Thr Leu Leu Leu Ala Val Ala Val Leu Phe Pro Tyr Met
27 10 15 20 25
28 acg gaa cca gca caa gcc cat cat aat ggg acg aat ggg acc atg atg 267
29 Thr Glu Pro Ala Gln Ala His His Asn Gly Thr Asn Gly Thr Met Met
30 30 35 40
31 cag tat ttt gaa tgg cat ttg cca aat gac ggg aac cac tgg aac agg 315
32 Gln Tyr Phe Glu Trp His Leu Pro Asn Asp Gly Asn His Trp Asn Arg
33 45 50 55
34 tta cga gat gac gca gct aac tta aag agt aaa ggg att acc gct gtt 363
35 Leu Arg Asp Asp Ala Ala Asn Leu Lys Ser Lys Gly Ile Thr Ala Val
36 60 65 70
37 tgg att cct cct gca tgg aag ggg act tcg caa aat gat gtt ggg tat 411
38 Trp Ile Pro Pro Ala Trp Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr
39 75 80 85
40 ggt gcc tat gat ttg tac gat ctt ggt gag ttt aac caa aag gga acc 459
41 Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr
42 90 95 100 105
43 gtc cgt aca aaa tat ggc aca agg agt cag ttg caa ggt gcc gtg aca 507
44 Val Arg Thr Lys Tyr Gly Thr Arg Ser Gln Leu Gln Gly Ala Val Thr
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45		110	115	120	
46	tct ttg aaa aat aac ggg att caa gtt tat ggg gat gtc gtg atg aat	555			
47	Ser Leu Lys Asn Asn Gly Ile Gln Val Tyr Gly Asp Val Val Met Asn				
48		125	130	135	
49	cat aaa ggt gga gca gac ggg aca gag atg gta aat gcg gtg gaa gtg	603			
50	His Lys Gly Gly Ala Asp Gly Thr Glu Met Val Asn Ala Val Glu Val				
51		140	145	150	
52	aac cga agc aac cga aac caa gaa ata tca ggt gaa tac acc att gaa	651			
53	Asn Arg Ser Asn Arg Asn Gln Glu Ile Ser Gly Glu Tyr Thr Ile Glu				
54		155	160	165	
55	gca tgg acg aaa ttt gat ttc cct gga aga gga aat acc cat tcc aac	699			
56	Ala Trp Thr Lys Phe Asp Phe Pro Gly Arg Gly Asn Thr His Ser Asn				
57		170	175	180	185
58	ttt aaa tgg cgc tgg tat cat ttt gat ggg aca gat tgg gat cag tca	747			
59	Phe Lys Trp Arg Trp Tyr His Phe Asp Gly Thr Asp Trp Asp Gln Ser				
60		190	195	200	
61	cgt cag ctt cag aac aaa ata tat aaa ttc aga ggt acc gga aag gca	795			
62	Arg Gln Leu Gln Asn Lys Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala				
63		205	210	215	
64	tgg gac tgg gaa gta gat ata gag aac ggc aac tat gat tac ctt atg	843			
65	Trp Asp Trp Glu Val Asp Ile Glu Asn Gly Asn Tyr Asp Tyr Leu Met				
66		220	225	230	
67	tat gca gac att gat atg gat cat cca gaa gta atc aat gaa ctt aga	891			
68	Tyr Ala Asp Ile Asp Met Asp His Pro Glu Val Ile Asn Glu Leu Arg				
69		235	240	245	
70	aat tgg gga gtt tgg tat aca aat aca ctt aat cta gat gga ttt aga	939			
71	Asn Trp Gly Val Trp Tyr Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg				
72		250	255	260	265
73	atc gat gct gtg aaa cat att aaa tac agc tat acg aga gat tgg cta	987			
74	Ile Asp Ala Val Lys His Ile Lys Tyr Ser Tyr Thr Arg Asp Trp Leu				
75		270	275	280	
76	aca cat gtg cgt aac acc aca ggt aaa cca atg ttt gca gtt gca gaa	1035			
77	Thr His Val Arg Asn Thr Thr Gly Lys Pro Met Phe Ala Val Ala Glu				
78		285	290	295	
79	ttt tgg aaa aat gac ctt gct gca atc gaa aac tat tta aat aaa aca	1083			
80	Phe Trp Lys Asn Asp Leu Ala Ala Ile Glu Asn Tyr Leu Asn Lys Thr				
81		300	305	310	
82	agt tgg aat cac tcc gtg ttc gat gtt cct ctt cat tat aat ttg tac	1131			
83	Ser Trp Asn His Ser Val Phe Asp Val Pro Leu His Tyr Asn Leu Tyr				
84		315	320	325	
85	aat gca tct aat agt ggt ggc tat ttt gat atg aga aat att tta aat	1179			
86	Asn Ala Ser Asn Ser Gly Gly Tyr Phe Asp Met Arg Asn Ile Leu Asn				
87		330	335	340	345
88	ggt tct gtc gta caa aaa cac cct ata cat gca gtc aca ttt gtt gat	1227			
89	Gly Ser Val Val Gln Lys His Pro Ile His Ala Val Thr Phe Val Asp				
90		350	355	360	
91	aac cat gac tct cag cca gga gaa gca ttg gaa tcc ttt gtt caa tcg	1275			
92	Asn His Asp Ser Gln Pro Gly Glu Ala Leu Glu Ser Phe Val Gln Ser				
93		365	370	375	
94	tgg ttc aaa cca ctg gca tat gca ttg att ctg aca agg gag caa ggt	1323			

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95      Trp Phe Lys Pro Leu Ala Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly
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97      tac cct tcc gta ttt tac ggt gat tac tac ggt ata cca act cat ggt      1371
98      Tyr Pro Ser Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly
99              395              400              405
100     gtt cct tcg atg aaa tct aaa att gat cca ctt ctg cag gca cgt caa      1419
101     Val Pro Ser Met Lys Ser Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln
102     410              415              420              425
103     acg tat gcc tac gga acc caa cat gat tat ttt gat cat cat gat att      1467
104     Thr Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe Asp His His Asp Ile
105              430              435              440
106     atc ggc tgg acg aga gaa ggg gac agc tcc cac cca aat tca gga ctt      1515
107     Ile Gly Trp Thr Arg Glu Gly Asp Ser Ser His Pro Asn Ser Gly Leu
108              445              450              455
109     gca act att atg tcc gat ggg cca ggg ggt aat aaa tgg atg tat gtc      1563
110     Ala Thr Ile Met Ser Asp Gly Pro Gly Gly Asn Lys Trp Met Tyr Val
111              460              465              470
112     ggg aaa cat aaa gct ggc caa gta tgg aga gat atc acc gga aat agg      1611
113     Gly Lys His Lys Ala Gly Gln Val Trp Arg Asp Ile Thr Gly Asn Arg
114              475              480              485
115     tct ggt acc gtc acc att aat gca gat ggt tgg ggg aat ttc act gta      1659
116     Ser Gly Thr Val Thr Ile Asn Ala Asp Gly Trp Gly Asn Phe Thr Val
117     490              495              500              505
118     aac gga ggg gca gtt tcg gtt tgg gtg aag caa taaataagga acaagaggcg      1712
119     Asn Gly Gly Ala Val Ser Val Trp Val Lys Gln
120              510              515
121     aaaattactt tcctacatgc agagctttcc gatcactcat acaccaata taaattggaa      1772
122     gctt      1776
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124 <211> LENGTH: 516
125 <212> TYPE: PRT
126 <213> ORGANISM: Bacillus sp.
127 <400> SEQUENCE: 2
128     Met Lys Leu His Asn Arg Ile Ile Ser Val Leu Leu Thr Leu Leu Leu
129           1              5              10              15
130     Ala Val Ala Val Leu Phe Pro Tyr Met Thr Glu Pro Ala Gln Ala His
131           20              25              30
132     His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His Leu
133           35              40              45
134     Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala Asn
135           50              55              60
136     Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp Lys
137           65              70              75              80
138     Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp
139           85              90              95
140     Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr
141           100             105             110
142     Arg Ser Gln Leu Gln Gly Ala Val Thr Ser Leu Lys Asn Asn Gly Ile
143           115             120             125
144     Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp Gly

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145          130          135          140
146  Thr Glu Met Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn Gln
147  145          150          155          160
148  Glu Ile Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp Phe
149          165          170          175
150  Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr His
151          180          185          190
152  Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys Ile
153          195          200          205
154  Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp Ile
155          210          215          220
156  Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met Asp
157  225          230          235          240
158  His Pro Glu Val Ile Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr Thr
159          245          250          255
160  Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His Ile
161          260          265          270
162  Lys Tyr Ser Tyr Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr Thr
163          275          280          285
164  Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu Ala
165          290          295          300
166  Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val Phe
167  305          310          315          320
168  Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly Gly
169          325          330          335
170  Tyr Phe Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys His
171          340          345          350
172  Pro Ile His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro Gly
173          355          360          365
174  Glu Ala Leu Glu Ser Phe Val Gln Ser Trp Phe Lys Pro Leu Ala Tyr
175          370          375          380
176  Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr Gly
177  385          390          395          400
178  Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ser Met Lys Ser Lys
179          405          410          415
180  Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Tyr Ala Tyr Gly Thr Gln
181          420          425          430
182  His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu Gly
183          435          440          445
184  Asp Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp Gly
185          450          455          460
186  Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys His Lys Ala Gly Gln
187  465          470          475          480
188  Val Trp Arg Asp Ile Thr Gly Asn Arg Ser Gly Thr Val Thr Ile Asn
189          485          490          495
190  Ala Asp Gly Trp Gly Asn Phe Thr Val Asn Gly Gly Ala Val Ser Val
191          500          505          510
192  Trp Val Lys Gln
193          515
194  <210> SEQ ID NO 3

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195 <211> LENGTH: 22
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197 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: any n = a,c,t or g
200 <220> FEATURE:
201 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
202 <400> SEQUENCE: 3
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205 <211> LENGTH: 26
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: any n = a,c,t or g
210 <220> FEATURE:
211 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
212 <400> SEQUENCE: 4
W--> 213      tcrtgtrtrt cnacraangt nacngc                                26
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215 <211> LENGTH: 23
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
220 <400> SEQUENCE: 5
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222 <210> SEQ ID NO 6
223 <211> LENGTH: 22
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
228 <400> SEQUENCE: 6
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233 <213> ORGANISM: Artificial Sequence
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235 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
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241 <213> ORGANISM: Artificial Sequence
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243 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
244 <400> SEQUENCE: 8

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VERIFICATION SUMMARY
PATENT APPLICATION US/08/952,741

DATE: 09/11/98
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Line	Error/Warning	Original Text
203	W "N" or "Xaa" used: Feature required	tngaygcngt naarcayath aa
213	W "N" or "Xaa" used: Feature required	tcrtgrttrt cnacraangt nacngc